

## ABSTRACT

Quantitative methods for analyzing measurement errors from nucleic acid arrays are provided. The methods are based on a two component model that approximates a constant standard deviation for very low expression levels, and  
5 constant relative standard deviation (RSD) for higher concentrations. Estimates of some model parameters may be obtained without resort to replicated measurements. Also provided are thresholding methods for establishing boundaries between low expression levels, high expression levels, and intermediate expression levels, and methods for estimating actual expression levels from intensity measurements.